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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

May 16, 2005, 17:16:07; Search time 162 Seconds (without alignments) 128.920 Million cell updates/sec

US-10-644-927-1 304 Title: Perfect score:

1 KTYYGINGVHCTKNSLWGKV.....GRLQDILLGWATGAFGKTFH 54 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 08
Maximum Match 1008 Minimum DB seq length: 0 Aaximum DB seq length: 2000000000

Listing first 45 summaries A_Geneseq_16Dec04:* Database

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003ss:* geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		*				
Result No.	Score	Query Match	o Ouery Match Length DB	DB	ID	Description
-	69.5	22.9	420	9	ADA33974	Ada33974 Acinetoba
7	64	21.1	61	~	AAW17990	
m ,	62.5	20.6	558	œ	ADR89438	
4	62	20.4	42	~	AAW11633	Aaw11633 Lactobaci
Ω.	9	19.7	37	~	AAW66446	Aaw66446 Cationic
9	9	19.7	37	٣	AAY91745	Aay91745 Cationic
7	9	19.7	300	~	AAR56481	_
æ	9	19.7	300	~	AAW37928	Aaw37928 Amino aci
6	9	19.7	300	4	AAB69069	Aab69069 Human CD3
10	9	19.7	300	ഗ	ABG61817	Abg61817 Prostate
11	9	19.7	300	9	ABU09711	Abu09711 CD38 prot
12	9	19.7	300	9	ABU09714	
13	9	19.7	300	7	ADD18904	
14	09	19.7	300	7	ADD45262	Add45262 Human Pro
15	9	19.7	300	7	ADN40030	Adn40030 Cancer/an
16	9	19.7	300	œ	ADM32177	Adm32177 Human CD3
17	9	19.7	300	œ	ADQ59526	Adq59526 Human can
18	9	19.7	300	œ	ADQ88192	
19	9	19.7	689	4	ABG06883	
20	59.5	19.6	513	~	AAW79755	Aaw79755 Euphorbia
21	59	19.4		N	AAR14564	Aar14564 Bacterioc
22	59	19.4	44	~	AAR91745	Aar91745 Brevicin,
23	59	19.4		~	AAR25078	Aar25078 PA-1 bact
24	59	19.4	300	9	ABU09712	Abu09712 CD38 prot
25	59	19.4	399	80	. ADN23488	Adn23488 Bacterial

Aab50093 GB1 prote	Adc64559 Trichodes	Adq07360 Trichodes	Abb 11088 Drosophil	Abu44608 Protein e	Abm69065 Photorhab	Abb05473 Enterocin	Adf04643 Bacterial	Adc95053 E. faeciu	Abu42656 Protein e	Abp38314 Staphyloc		Ads04803 Staphyloc	Aay06359 Fusarium	Aay84337 Amino aci	Aab14872 Fusarium	Aau77580 F. javani	Aau77424 Fusarium	Add46266 Rat Prote	Ade62845 Rat Prote
AAB50093	ADC64559	ADQ07360	ABB71088	ABU44608	ABM69065	ABB05473	ADF04643	ADC95053	ABU42656	ABP38314	ADO84851	ADS04803	AAY06359	AAY84337	AAB14872	AAU77580	AAU77424	ADD46266	ADE62845
4	7	œ	4	9	9	Ŋ	7	7	9	Ŋ	æ	8	7	ო	ო	Ŋ	ß	7	7
753	461	461	643	581	1565	45	242	99	6641	10182	10203	10203	244	244	244	244	244	1382	1382
19.4	18.9	18.9	18.9	18.8	18.8	18.6	18.6	18.4	18.4	18.4	18.4	18.4	18.3	18.3	18.3	18.3	18.3	18.3	18.3
29	57.5	57.5	57.5	57	57	56.5	56.5	26	. 26	26	26	26	55.5	55.5	55.5	55.5	55.5	55.5	55.5
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Acinetobacter baumannii; bacterial disease; antibacterial; vaccine; plant biocontrol agent. Acinetobacter baumannii protein #1135. ADA33974 standard; protein; 420 AA. (GENO-) GENOME THERAPEUTICS CORP. 99US-00328352. 98US-0088701P. (first entry) Acinetobacter baumannii. Breton G, Bush D; US6562958-B1. 04-JUN-1999; 09-JUN-1998; 20-NOV-2003 13-MAY-2003 ADA33974; RESULT 1 ADA33974

New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for plants

WPI; 2003-576092/54. N-PSDB; ADA29848.

Example; SEQ ID NO 5261; 328pp; English.

The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A. baumannii protein.

Sequence 420 AA;

4

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This polypeptide comprises the sakacin C bacteriocin of Lactobacillus sake LTH673 encoded by gene P (see AAT67149). The invention relates to the discovery of a new regulatory mechanism for gene expression in lactic acid bacteria that includes novel, strongly regulatable promoter elements (see AAT67142-48), such as that of the P gene. Expression of genes under the control of such promoters can be induced by addition of a bacteriocin inducing peptide such as the claimed peptide of L. sake (see AAM77989) or Lactobacillus plantarum (see AAM77989). Typical applications are in production of specific proteins, or where the bacteria express a surface antigen, as vaccines. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene expression system providing regulated lactic acid bacteria protein production - uses new inducing peptide involved in bacteriocin synthesis, useful in fermentation and as a drug delivery system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IF gene; gene expression; promoter; lactic acid bacterium; bacteriocin; vaccine; vector; sakacin P; ss.
                                                                                         Gaps
                                                                                                                                                                                      44
                                                                                         11;
                                                                                                                                             1 KTYYGTN---GVHCTKNSLWGKVRLKNMKY--DQNTTYMGRLQDI---LLGW
5; DB 6; Length 420;
3.9;
                                                                                      13; Indels
      22.9%; Scor.
38.5%; Pred. No. 5...
"... 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactobacillus sakei; strain LTH 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .18
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brurberg MB;
                                                                                                                                                                                                                                                                                                                                                            AAW17990 standard; protein; 61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19. .61
/label= Sakacin-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Fig 3; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-NO000266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95NO-00004575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                      20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIJSINK V G H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eijsink VGH, Nes IF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRUR/) BRURBERG M B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-289292/26.
N-PSDB; AAT67149.
                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9718316-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-OCT-2003
10-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sakacin P.
                                                                                                                                                                                                                                                                                                                                                                                                                    AAW17990;
                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EIJS/) (NESI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                      Matches
                                                                                                                                                                                                                                                                                               RESULT 2

AAW17990

DAW17990

AAW17990

AAW17990

AAW17990

AAW17990

AAW17990

AAW17990

AAW17990

AAW17990

AAW17990

AAW1790

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AAW1790

AAW1790

AAW113-1

AAW1790

AAW1790
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expression cassette, transformation, transgenic; plant, bacteria;
lepidoptera, coleoptera, pest, pesticide, resistance,
         20 YYG-NGVHCGKHSCTVDWG------TAIGNIGNNAAANWATG 54
3 YYGINGVHCIKNSL---WGKVRLKNMKYDQNTIYMGRL-QDILLGWAIG 47
                                                                                                                   delta-endotoxin; delta-endotoxin associate polypeptide;
                                                                                                                                                                                                                                                                                                                                        Carr B;
                                                                                                                                                                                                                                                                                                                                         Duck NB,
                                                       Ź
                                                                                                                                                                                                                                                                                                                                         Koziel MG,
                                                      ADR89438 standard; protein; 558
                                                                                                                                                                                                                           2003US-0448633E.
2003US-0448797P.
2003US-0448810P.
2003US-04488110P.
2004US-0078129.
2004US-00782020.
2004US-00782096.
2004US-00782570.
2004US-00782570.
                                                                                                                                                                                                       20-FEB-2004; 2004WO-US005829
                                                                                                                                                         Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                         Carozzi N, Hargiss T,
                                                                                                                                                                                                                                                                                                                          (ATHE-) ATHENIX CORP.
                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-635574/61.
                                                                                                                                           pesticidal activity
                                                                                                                                                                         WO2004074462-A2
                                                                                                     crybun2-orf2.
                                                                                                                                                                                                                                                                                           19-FEB-2004;
19-FEB-2004;
                                                                                                                                                                                                                                                                                                          19-FEB-2004;
                                                                                                                                                                                                                                      20-FEB-2003;
                                                                                                                                                                                                                                             20-FEB-2003;
                                                                                                                                                                                                                                                             20-FEB-2003;
                                                                                                                                                                                                                                                     20-FEB-2003;
                                                                                                                                                                                                                                                                    19-FEB-2004;
                                                                                                                                                                                                                                                                                    19-FEB-2004;
                                                                                                                                                                                                                               20-FEB-2003;
                                                                                     18-NOV-2004
                                                                                                                                                                                        02-SEP-2004
                                                                      ADR89438;
                                                ADR89438
               셤
```

This sequence represents a delta-endotoxin crystal protein. This protein was included in the scope of the invention as a comparison to the delta-endotoxins of the invention. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or

New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.

Example 6; SEQ ID NO 50; 178pp; English.

Sequence 558 AA;

Query Match

4

Gaps

18;

21.1%; Score 64; DB 2; Length 61; 36.7%; Pred. No. 1.9; ive 4; Mismatches 9; Indels

Query Match
Best Local Similarity 36.7
Matches 18; Conservative

Sequence 61 AA;

20.6%; Score 62.5; DB 8; Length 558;

Indolicidin analogue, resistance, cationic peptide, antibiotic, bacterial infection, tolerance, antibacterial, microorganism, bacteria,

fungus; parasite; virus.

WO9840401-A2

Cationic peptide leukocin A-val 187,

(first entry)

```
New indolicidin peptide analogues - useful for, e.g. enhancing activity of antibiotic or overcoming tolerance, acquired resistance or inherent resistance of microorganisms.
                                                                                                                                                                                                                                                                                                                          WPI; 1998-520800/44.
                                                                                                                     Leuconostoc gelidum
                                                                                                                                                                                                                           20-AUG-1997;
26-SEP-1997;
25-PEB-1998;
                                                                                                                                                                                           10-MAR-1998;
                          12-JAN-1999
                                                                                                                                                                  17-SEP-1998
                                                                                                                                                                                                                                                                                                    Fraser JR,
  AAW66446;
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
              3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is bacteriocin from a Lactobacillus strain [L. plantarum BN85 (DSM 9296)], which is derived from soft cheese. A partial fragment derived by Edman degradation (AAWIL1632) is capable of inhibiting growth of Listeria bacteria in cheese at the start of ripening. The new Lactobacillus strain is useful for prodn. Of Listeria-free cheese, pref. washed-rind cheese, esp. Wunster cheese. Strain DSM 9296 is added to the cheese during ripening, e.g. by spraying the cheese with a soln. contg. 104-106 cfu/ml of Lactobacillus. DSM 9296 is thibiting Listeria monocytogenes 1/2a, 1/2b, 1/2c, 3a, 3b, 4b, 4d and V7; Listeria innocus for and 6b; Listeria seeligeri; and Listeria ivanovii. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactobacillus strain that inhibits Listeria - for use in cheese prodn.
              Gaps
                                                                                                                                                                                                                          bacteriocin; Lactobacillus plantarum BN85; DSM 9296; soft cheese;
inhibitor; growth; ripening; washed-rind; Munster; L. monocytogenes;
L. innocua; L. seeligeri; L. ivanovii; Listeria.
                                                 26 IECMSNEHSSKEEMMLWDEVKQAKQLSWSRNLLYNGDFEDVSNGWKT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.4%; Score 62; DB 2; Length 42; ilarity 39.1%; Pred. No. 2.2; Conservative 6; Mismatches 8; Indels
                                  9 VHCTKNS-----LWGKVR-LKNMKYDQNTTYMGRLQDILLGWAT
            17; Indels
27.7%; Pred. No. 43; cive 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SA.
                                                                                                                                                                                                     Lactobacillus plantarum bacteriocin.
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FROM-) FROMAGERIE SIFFERT FRERES
                                                                                                                    AAW11633 standard; protein; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 32; 53pp; German.
                                                                                                                                                                                                                                                                                                                                      /note= "Cys-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                   96DE-02016369
                                                                                                                                                                                                                                                                                                                                                                                                            96DE-02016369
                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003 to correct PR field.
            13; Conservative
                                                                                                                                                                                                                                                                         Lactobacillus plantarum.
                                                                                                                                                                                                                                                                                                             9. .24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-088733/09
 Best Local Similarity
                                                                                                                                                                                                                                                                                                             Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42 AA;
                                                                                                                                                                                                                                                                                                                                                              DE29616369-U1
                                                                                                                                                                                                                                                                                                                                                                                                          20-SEP-1996;
                                                                                                                                                                 25-MAR-2003
05-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                   20-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-1997.
                                                                                                                                           AAW11633;
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             Matches
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Mcnicol PJ

West MHP,

(MICR-) MICROLOGIX BIOTECH INC.

97US-0040649P. 97US-00915314. 97US-0060099P. 98US-00030619.

10-MAR-1997;

98WO-CA000190.

```
AAW66193 to AAW66469 represent native cationic peptides from the present invention. The present invention describes compositions and methods for treating infection, especially bacterial infections. The compositions and methods use cationic peptides in combination with an antibiotic agent which are then administered to a patient to enhance the activity of the antibiotic agent, to overcome: (a) tolerance; (b) acquired resistance; peptides can provide synergistic activity against a microorganism that is tolerant, inherently resistant, or has acquired resistance to an antibiotic agent. They can be used for killing e.g. bacteria, fungi, parasites and viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; bleakeamia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon; multidrug resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cationic peptide Leukocin A-val 187 amino acid seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YYG-NGVHCTKSGCSVNWGBAFSAGVHRLAN 31
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
19.7%; Score 60; DB
Best Local Similarity 48.4%; Pred. No. 3.5;
Matches 15; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 YYGTNGVHCTKNSL---WGKV-----RLKN 24
Disclosure, Page 11; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z
                                                                                                                                                                                                                                                                                                                                                                            Sequence 37 AA;
```

Gaps

14;

Local Similarity tes 18; Conserv

YYG-NGVTCGKHSVDWGKA-----TTCI--INNGAMAWATG 34 3 YYGTNGVHCTKNSL-WGKVRLKNMKYDQNTTYMGRLQDILLGWATG 47

AAW66446 standard; peptide; 37 AA.

AAW66446 ID AAW6 XX

RESULT 5

유 8

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113 GTQTVPCNKILLMSRIKDLAHQFTQVQRDMFTLEDTLLGY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 8-10; 17pp; Japanese.
                                                          Disclosure; Page 46; 54pp; English.
                                                                                                                                                                                                                                                                                                              AAW37928 standard; protein; 300 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-JP001259
                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of CD38.
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                        Query Match
Best Local Similarity 35.09
Watches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-251054/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV29155
                                                                                                                                                       Sequence 300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9816245-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                            09-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          raminato T;
                                                                                                                                                                                                                                                                                                                                      AAW37928;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                   AAW37928
                                                                                                                                                                                                                                                                                        RESULT
 셤
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                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                       Э.
                                                                                                                                                                                                                                               This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO) emodified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multiding resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon
                                                                                                                                                                                                       treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heath A;
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                            West
                                                                                                                                                                                        Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating 1
                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bazan JF,
                                                                                                                                           Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                              19.7%; Score 60; DB 3; Length 37; 48.4%; Pred. No. 3.5; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grimaldi JC,
                                                                                                                                           Erfle D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 YYG-NGVHCTKSGCSVNWGEAFSAGVHRLAN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                             3 YYGTNGVHCTKNSL---WGKV-----RLKN 24
                                                                                                                                           Taylor R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCHE ) SCHERING CORP. (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhouse RME, Santos-Argumedo L,
Howard MC, Goodnow CC;
                                                                                                                                                                                                                             Disclosure, Page 11, 94pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR56481 standard; protein; 300 AA
                                                                                                                   (MICR-) MICROLOGIX BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD38; therapeutic; diagnostic
                                                                     99WO-CA000552
                                                                                            98US-00096541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US000517
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                                                                                                                                           Friedland HD, Krieger TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                   WPI; 2000-223549/19.
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-264098/32.
N-PSDB; AAQ70644.
                                                                                                                                                                                                                                                                                                                                                                         Sequence 37 AA;
Unidentified
                       WO9965506-A2
                                                                                             .2-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-1994;
                                                                     14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9417184-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
22-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR56481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD38.
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ID AAR
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Modulation of responses of lymphocytes - using antibody to CD38, a soluble CD38 fragment or a modulator of ADP-ribosyl cyclase or cyclic ADP-ribosyl hydrolase.
                                                                                                                                                                             The protein is a human CD38 molecule which is used to modulate the physiological response of a lymphocte, which is useful for the stimulation/inhibition of lymphocyte growth or differentiation, particularly for the establishment of antigen tolerance. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the amino acid sequence of the CD38 protein, of which a fragment is used in the method of the invention to create the anti-CD38 autoantibody. The method is used for detecting autoimmune disease, e.g. insulin dependent diabetes mellitus or type II diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD38; CD38 peptide fragment; anti-CD38 autoantibody; autoimmune disease; insulin dependent diabetes mellitus; type II diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assaying anti-CD38 auto-antibody - useful for detecting auto-immune disease, e.g. type II diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                                                                                                                                                                                                                                                                             19.7%; Score 60; DB 2
35.0%; Pred. No. 43;
tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.7%; Score 60; DB
35.0%; Pred. No. 43;
tive 7; Mismatches
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13-OCT-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae.
                                                                                                Gish KC,
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                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
#X#X6X#X8X#X6X#X
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                                                                                                                                                                                                                                                                          The present invention describes a method using a mutation in the CD38 gene (involved in the production of cyclic ADP-ribose (cADPR)), to detect the onset of diabetes mellitus. The method is useful for detecting the onset of diabetes mellitus. The present sequence represents human CD38, which is used in an example from the present invention
                                                                                                                                                                                                                                  Detecting onset of diabetes mellitus comprises detecting specific gene mutations in the CD38 gene.
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                        Human; CD38; diabetes mellitus; detection; cyclic ADP-ribose; cADPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
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                                                                                                                                                                                                                                                                                                                                     19.7%; Score 60; DB 4; Length 300; 35.0%; Pred. No. 43; tive 7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                              5 GINGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGW 44
                                                                         Human CD38 protein seguence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prostate cancer-associated protein #18
                                                                                                                                                                                                                                                            Example, Page 11-12, 19pp, Japanese.
                             AAB69069 standard; protein; 300 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                          ABG61817 standard; protein; 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2001; 2001WO-US032045.
                                                                                                                                                   99JP-00131955
                                                                                                                                                                   99JP-00131955
                                                          (first entry)
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                                                                                                                                                                                                                WPI; 2001-128255/14.
N-PSDB; AAF32487.
                                                                                                                                                                                  BML KK.
KANETSUKA A.
                                                                                                                                                                                                 OKAMOTO H.
                                                                                                                                                                                                                                                                                                                        Sequence 300 AA;
                                                                                                                       JP2000316578-A.
                                                                                                                                                                   12-MAY-1999;
                                                                                                        Homo sapiens
                                                                                                                                                    12-MAY-1999;
                                                                                                                                     21-NOV-2000.
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. Best Local S:
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                    113
                                           AAB69069
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG61817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia
                                                                                                                                                                                 (BMLB-)
(KANE/)
                                                                                                                                                                                                 (OKAM/)
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                   RESULT 9
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The present invention relates to methods of detecting a prostate cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancerassociated polymuclectides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The hybridise to a sequence that is at least 80% identical to them. The constant cancerassociated polymuclectide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals of e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancerase as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABG61800-ABG61944 represent prostate cancer-associated proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.7%; Score 60; 35.0%; Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                         Wilson KE,
2000US-00733288.

2000US-0073742.

2001US-02539579.

2001US-027691P.

2001US-0281922P.

2001US-0286214P.

2001US-0286214P.
                                                                                                                                                                                                                                                                                                  (EOSB-) EOS BIOTECHNOLOGY INC
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                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-471335/50.
                                                                                                                                                                                                                                                                                                                                                            Mack DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABK92132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostate tissue
                                                                                    16-MAR-2001;
16-MAR-2001;
06-APR-2001;
                                                                                                                                                                            24-APR-2001;
                                                                                                                                                                                                                                         04-MAY-2001;
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                                                            24-JAN-2001;
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(NAGA/) (SAGE/) (MATS/)

EGAS/)

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The invention describes a method of detecting a risk factor for diabetic onset in an individual. The method involves detecting genetic abnormality of the gene CD38 which is a human lymphocyte surface marker and is a risk gene for onset of diabetes. The sites of abnormality in CD38 gene include a site encoding Arg at residue 140, a site encoding Ser at residue 264, or guanine at nucleotide position -28 in intron 7. This is the amino acid sequence of CD38 protein S264k mutant that results from a mutation in the gene encoding CD38, a risk factor in the onset of diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; disease state; cytostatic; antiinflammatory; ophthalmological; antiarteriosclerotic; vulnerary; gene therapy; phypoxia-regulated condition; tumourigenesis; anglogenesis; apoptosis; inflammation; erythropoiesis; glycolygis; gluconeogenesis; glucose transportation; catecholamine synthesis; iron transport; nitic cancer; ischaemic condition; reperfusion injury; retinopathy; neonatal stress; pre-eclampsia; atherosclerosis; inflammatory condition; wound healing.
                                                                                                                                         Detecting risk factor for onset of diabetes in an individual, involves detecting genetic abnormality of the gene CD38.
                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Length 300;
                                                    Matsui K, Hattori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ward NR, Harris RA, Naylor S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GINGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGW
                                                                                                                                                                                                                                                                                                                                                                                                                                 19.7%; Score 60; DB 35.0%; Pred. No. 43; tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human disease related protein SegID393.
                                                Sagehashi Y,
3, Okamoto H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD18904 standard; protein; 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-2001; 2001GB-00020558.
05-OCT-2001; 2001GB-00024037.
                                                                                                                                                                                                 Example; Page; 29pp; English
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                                                    Nagano M,
Takasawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-290046/28.
N-PSDB; ADD18905.
                                                                                                           WPI; 2003-417248/39
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 300 AA;
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                                                    Egashira T,
Kanatsuka A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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(TAKA/)
(OKAM/)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                             The invention describes a method of detecting a risk factor for diabetic onset in an individual. The method involves detecting genetic abnormality of the gene CD38 which is a human lymphocyte surface marker and is a risk gene for onset of diabetes. The sites of abnormality in CD38 gene include a site encoding Arg at residue 140, a site encoding Ser at residue 264, or guanine at nucleotide position -28 in intron 7. This is the amino acid sequence of wild type CD38 protein
                                                                                                                                                                                                                                                                              Detecting risk factor for onset of diabetes in an individual, involves detecting genetic abnormality of the gene CD38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD38; diabetic onset; diabetes; lymphocyte surface marker; mutant;
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                                                                                                                                                                                  Hattori H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
19.7%; Score 60; DB 6; Length 300;
Best Local Similarity 35.0%; Pred. No. 43;
Matches 14; Conservative 7; Mismatches 19; Indels
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                                                                                                                                                                                  Mateui K,
                                                                                                                                                                                Sagehashi Y,
3, Okamoto H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 10; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU09714 standard; protein; 300 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JAN-2001; 2001US-00773307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2001; 2001US-00773307
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                                                                                                                                                                                Nagano M,
Takasawa (
                                                                     MATSUI K.
HATTORI H.
KANATSUKA A.
TAKASAWA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGASHIRA T.
NAGANO M.
SAGEHASHI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MATSUI K.
HATTORI H.
KANATSUKA A.
                                 NAGANO M.
SAGEHASHI Y.
                                                                                                                                                                                                                                       WPI; 2003-417248/39.
                                                                                                                                              OKAMOTO H.
                                                                                                                                                                                                                                                          N-PSDB; ACA60951.
                EGASHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 300 AA;
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                                                                                                                                                                                                   Kanatsuka A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2003
                                                                                                                                                                                Egashira T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU09714;
                                                                                                         (KANA/)
(TAKA/)
(OKAM/)
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(NAGA/)
(SAGE/)
(MATS/)
(HATT/)
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RESULT 12 ABU09714

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                                            This invention relates to novel human genes and gene product which are implicated in certain disease states. Compounds which modulate the proteins of the invention may here cytostatic, antinflammatory, ophthalmological, antiateriosclerotic or vulnerary activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for gene therapy. The invention may be useful for diagnosing or treating a hypoxia-regulated condition, such as tumourigenesis, angiogenesis, apoptosis, inflammation, erythropolesis, or the biological response to hypoxia conditions including processes such as glycolysis, gluconegenesis, glucone transportation, catecholamine synthesis, iron transport or nitric oxide synthesis. The disease includes cancer, ischaemic conditions, reperfusion injury, retinopathy, meonatel stress, pre-eclampsia, atherosclerosis, inflammatory conditions or wound healing. The present sequence is that of a disease related protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                 Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, pain, neuronal tissue, gene therapy,
spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
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                                                                                                                                                                                                                                                    19.7%; Score 60; DB 7; Length 300; 35.0%; Pred. No. 43; tive 7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                    S GINGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGW 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Costigan M;
                      Claim 25; SEQ ID NO 393; 424pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Protein P28907, SEQ ID NO 10695.
                                                                                                                                                                                                                                                                                                                                                                                          ADD45262 standard; protein; 300 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                  Local Similarity
nes 14; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-268312/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Woolf C, D'urso D,
                                                                                                                                                                                                                               Sequence 300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003016475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENBANK; P28907
 wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2004
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                                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                                                                                                                                                                                                                                                                                  ADD45262;
                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                            ADD45262
요
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Comprising the vector, a method for interportage a sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that increases are decreases the expression of a fortunially expressed or a first animal subjected to pain, a method for identifying a compound which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating activity in an animal of one or more of the polypeptides given in the appetidation, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene the sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed the sequence data for this patent did not form part of the printed the contraction which is differentially expressed during pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C400.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 GTQTVPCNKILLWSRIKDLAHQFTQVQRDMFTLEDTLLGY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 GINGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGW 44
a method for identifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60; DB 7
Pred. No. 43;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frp.wipo.int/pub/published_pct_sequences.
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2002US-0356714P.
2002US-0359077P.
2002US-0368809P.
2002US-0370110P.
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2001US-0340376P.
2002US-0347211P.
2002US-0347349P.
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35.0%;
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2001US-0334393P.
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Best Local Similarity 35.09
Matches 14, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 300 AA;
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29-MAR-2002;
04-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-2002;
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a confidence of determining the presence or absence of a pathological cell in a confidence or determining the presence or absence of the invention. The invention or by detecting a polypeptide of the invention. The concerts of the invention also relates to expression vectors and host cells comprising a concert acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; concerts and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atheroscalerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                          Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                        Gish KC, Glynne R, Hevezi PA; Wilson KE, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.7%; Score 60; DB 7; Length 300;
Best Local Similarity 35.0%; Pred. No. 43;
Matches 14; Conservative 7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; SEQ ID NO C400; 1385pp; English.
                                                                                                                                                                                                        Aziz N, Ginsburg WM,
Murray R, Watson SR,
12-APR-2002; 2002US-0372246P.
05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839P.
22-JUL-2002; 2002US-0397775P.
22-JUL-2002; 2002US-0397845P.
09-SEP-2002; 2002US-0409450P.
                                                                                                                                                              (EOSB-) EOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                         WPI; 2003-468649/44.
                                                                                                                                                                                                                                                                                                N-PSDB; ADN39813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 300 AA;
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Mack DH,
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113 GTQTVPCNKILLMSRIKDLAHQFTQVQRDMFTLEDTLLGY 152 엄

5 GINGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGW 44

Matches

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Gaps

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Search completed: May 16, 2005, 17:31:07 Job time : 166 secs

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Sequence 5, Appliance Sequence 44549, A Sequence 209, Appl Sequence 209, Appl Sequence 18807, A Sequence 4928, Appl Sequence 4928, Appl Sequence 3159, Appl Sequence 131, Appl Sequence 
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Sequence 43, Appl
Sequence 10, Appl
Sequence 1851, A
Sequence 23, Appl
Sequence 29, Appl
Sequence 29, Appl
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Sequence 454, App
Sequence 3, Appli
Sequence 5289, Ap
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 12, Appli
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13, Appi
43, Appi
70, Appi
18521, A
23, Appi
29, Appi
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183.230 Million cell updates/sec
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1 KTYYGINGVHCTKNSLWGKV......GRLQDILLGWATGAFGKTFH
                                                                                                                                                        May 16, 2005, 17:27:38 ; Search time 22 Seconds
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-068-507C-5

US-08-507C-5

US-08-270-744549

US-08-924-629C-69

US-09-030-619-209

US-09-030-619-209

US-09-244-629C-71

US-09-543-681A-4928

US-09-134-001C-3159

US-09-134-001C-3159

US-09-134-001C-3159

US-09-134-001C-3159

US-09-134-001C-3159

US-09-134-135-135

US-09-134-135-135

US-08-378-313-29

US-09-071-035-456

US-09-071-035-456
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US-08-032-848C-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           513545 segs, 74649064 residues
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Sequence Seq		ELATING	420;	-LLGW 44 : PLIGW 40	ITS USE	18;
		SEQUENCES RELATING ID THERAPEUTICS	Length 4 Indels	3RLQDI : RRLRDITSP		Length 61; ; Indels
S-09-216-295-24 S-09-632-570-24 S-09-632-575-54 S-09-311-170-6 S-09-131-170-6 S-09-248-796A-17748 S-09-26-104C-12 S-09-56-952-6 S-09-57-999-2 S-09-57-999-2 S-09-57-999-2 S-09-57-999-2 S-09-57-999-2 S-09-57-999-2 S-09-57-999-2 S-09-502-540-13820 S-09-902-540-11642 S-09-727-628-2 S-09-902-540-11642 S-09-727-628-2	ALIGNMENTS	s/09328352 : al. ACID AND AMINO ACID SEG. I FOR DIAGNOSTICS AND 'US/09/328,352 :-04	re 69.5; DB 4; d. No. 0.41; Mismatches 13;	LKNMKYDQNTTYMGRLQDILLGW 	IN MICROORGANISM AND HOMOLOGOUS PROTEINS 507C	re 64; DB 4; Le id. No. 0.2; Mismatches 9;
US-09-57 US-09-67 US-09-11 US-09-12 US-09-57 US-09-57 US-09-57 US-09-57 US-09-57 US-09-57 US-09-57 US-09-57 US-09-57 US-09-57	ALIG	09328352 al. CID AND ? FOR DIAN IS/09/328, 04	Sco Pre 8;	ρ _a ι	on US/09068507C VINCENT et al. EXPRESSION SYSTEM HTTEROLOGOUS AND -0.122P NUMBER: US/09/068, 1998-07-15 5: 12 fersion 3.1	Score 6 Pred. N
Ო ଫ ଫ Ო ଫ ଫ ଫ M H ଫ ଫ ଫ N ଫ ଫ ଫ ଫ		1 US/0932 1 et al. IIC ACID INNII FOR A A. R: US/09 1-06-04 12	54;	KAN31	0906 SION SION OLOG -07-	21.1%; 36.7%; ive
264 264 384 384 371 418 9110 219 229 249 2499 1390 360 59		5261 11, Application 1562958 1862958 18MATION: Breton WENTION: BUCKEI VENTION: BULMAN NEC: GTC9-03PA LICATION NUMBER LING DATE: 1999- 18EQ ID NOS: 8252 61	22.9%; illarity 38.5%; Conservative	KTYYGTNGVHCTKNSLWGKV :: :: ESVYVTNPKSGKHSNKANIWIK-	Application US/ 7790951 DRATION: DRATION: WENTION: HETER WVENTION: HETER WVENTION: HETER WYENTION: HORER BLICATION NUMBER LING DATE: 1998 SEQ ID NOS: 12 PALCATION VERSION	at
<u> </u>		plic 8 8 0N: 0N: 0N: NO: NO: LODE	rit) n8e	- ATT	cati 1 1 0 ON: NK, ON: 138C ION ION IN V	rity ngel
		-5261 61, Ap 656295 686295 0RMATI GARY NVENTI NVENTI NVENTI ENCE: PLICAT	E .	KTYYGTN- :: ESVYVTNP	C-5 Applicatio 6790951 FORMATION: INVENTION: INVENTION: ELING DATE: SEQ ID NOS: SEQ ID NOS: SEQ ID NOS: SECO ID NOS:	mila Co
6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		352- 40.6 10.6 10.6 10.6 10.6 11.4 11.4 11.4 11.4 11.4 11.4 11.4 11	atch cal 2	1 K?	Sequence 5, Application US/09068507C Sequence 5, Application US/09068507C Patent No. 6790951 GENERAL INFORMATION: TITLE OF INVENTION: EXPRESSION SYSTITILE OF INVENTION: HETEROLOGOUS AN FILE REFERENCE: 1380-0122 CURRENT FILING DATE: 1998-07-15 NUMBER OF SEQ ID NOS: 12 SEQ ID NO 5 EQ ID NOS: 12 SEQ ID NO 5 EXECUTE: 61 TYPE: PRT ORGANISM: Lactobacillus sake ORGANISM: Lactobacillus sake -09-068-507C-5	/ Match Local Similarity nes 18; Conserv
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		RESULT 1 US-09-328- Sequence Sequence Patent N GENERAL TITLE C	Query M Best Lo Matches	<u>ئ</u> ۾	RESULT 2 US-068-507C-5 Sequence 5, Ap Patent No. 679 GENERAL INFORM APPLICANT: EI TITLE OF INVE TITLE OF INVE FILE REFERENC CURRENT FILIN TUMBER OF SEQ SOFTWARE: PAT SEQ ID NO 5 LENGTH: 61 TYPE: PRT ORGANISM: La US-09-068-507C-5	Query Ma Best Loc Matches

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Sequence 68, Application US/08924629C

Sequence 68, Application US/08924629C

Sequence 68, Application US/08924629C

SERVERAL INFORMATION:
APPLICANT: Van Belkum, Marius J.
APPLICANT: Worobo, Randy W.
APPLICANT: Worobo, Randy W.
APPLICANT: McMullen, Lynn M.
APPLICANT: McMullen, Lynn M.
APPLICANT: Doon, Alson
APPLICANT: Lorser, G. Gordon
APPLICANT: Charles M.A.P.
TITLE OF INVENTION: No. 6403082elBacteriocins, Transport and Vector System and Method
TITLE OF INVENTION: No. 6403082elBacteriocins, Transport and Vector System and Method
TITLE OF INVENTION: No. 6403082elBacteriocins, Transport
CURRENT FILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: US 60/026,257

PRIOR APPLICATION NUMBER: US 60/026,257

PRIOR PILING DATE: 1996-09-05

NUMBER OF SEQ ID NOS: 80

SOFTWARER: PatentIn Version 3.1
SEG IN NO APPLICATION NOTE
                                                                                                                                                                                                                     APPLICANT: Fraes, Janet R.
APPLICANT: West, Michael H.P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FaetSEQ for Windows Version 3.0
SEQ ID NO 209
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 YYGINGVHCTKNSL---WGKV-----RLKN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 YYG-NGVHCTKSGCSVNWGEAFSAGVHRLAN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.7%; Score 60; DB Best Local Similarity 48.4%; Pred. No. 0.36 Matches 15; Conservative 2; Mismatches
                    Sequence 209, Application US/09030619B Patent No. 6503881
GENERAL INFORMATION:
                                                                                                                             Krieger, Timothy J.
Taylor, Robert
Erfle, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Leuconostoc gelidum
US-09-030-619-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Conservative
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Best Local Similarity
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US-09-248-796A-18807
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US-08-924-629C-68
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LENGTH: 61
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APPLICANT: Stiles Michael E.
APPLICANT: Stiles Michael E.
APPLICANT: Vederae, John C.
APPLICANT: Von Belkum, Marius J.
APPLICANT: Worobo, Rodney J.
APPLICANT: Worobo, Rodney J.
APPLICANT: McMullen, Lynn M.
APPLICANT: Beiner, Jorgen J.
APPLICANT: Poon, Alsian
APPLICANT: Franz, Charles M.A.P.
APPLICANT: Estenz, Charles M.A.P.
TITLE OF INVENTION: No. 6403082elBacteriocins, Transport and Vector System and Method
FILE REPERENCE: 660.005018
FILE REPERENCE: 660.005018
FILE REPERENCE: 1997-09-05
FRIOR PILING DATE: 1997-09-05
FRIOR PILING DATE: 1996-09-05
FRIOR FILING DATE: 1996-09-05
FRIOR FILING DATE: 1996-09-05
FRIOR FILING PAPEL PAPEL
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                                                                                                                                                                                                          Sequence 44549, Application US/09270767

Patent No. 670341

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFRENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

UNMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 44549

LENGTH: 85
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47
                                      20 YYG-NGVHCGKHSCTVDWG-----TAIGNIGNNAAANWATG 54
3 YYGINGVHCTKNSL---WGKVRLKNMKYDQNTTYMGRL-QDILLGWATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.4%; Score 62; DB 4; Length 85; ilarity 38.2%; Pred. No. 0.57; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 NACHCNKCSKWSYMXVYIRKYQQGSSEEGVLNDI 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 NGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDI 40
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Pred. No. 0.36;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 YYGTNGVHCTKNSL---WGKV-----RLKN 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 69, Application US/08924629C; Patent No. 6403082; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.7%;
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
.....hes 13; Conservat
                                                                                                                                                                                                US-09-270-767-44549
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ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
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Indels

10; Length 61; Indels DB 4; 19.7%; Score 60; DB 4 48.4%; Pred. No. 0.71; 26 YYG-NGVHCTKSGCSVNWGEAESAGVHRLAN 55 3 YYGINGVHCIKNSL---WGKV-----RLKN 24 2; Mismatches

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 49.28
LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4680, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                                                                                                                                                                                                                                                                                                                                         DOCATION: (18) COTHER INFORMATION: Identity of amino acid at the above locations are unknown. US-09-543-681A-4928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- MKYDQNTTYMGRLQDILLGWATGAF 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
FRIOR APPLICATION DATE: 30-Jun-1998
PRIOR APPLICATION DATE: 60/085,598
FRIING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INPORMATION:

NAME: Ariniello north
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Indels .17;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 12;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                        18.6%; Score 56.5; 28.1%; Pred. No. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100 Beaver, Street CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 YGTNGVHCTKNSLWGKVRLKN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4680:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                          ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.6
Best Local Similarity 28.1
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 ATIF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 GKTF 53
                                                                                                                                                                                                                                                                                                                      NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-09-107-532A-4680
                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                             FEATURE
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TILL OF INVENTION: No. 6403082elBacteriocins, Transport and Vector System and Method
FILE REFERENCE: 660.00508
CURRENT FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 60/026,257
PRIOR APPLICATION NUMBER: US 60/026,257
PRIOR PILING DATE: 1996-09-05
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 80
LENGTH: 62
TYPP: ...
Sequence 18807, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT PILING DATE: 1999-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ñ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 TTGVOCDESTLWVKL-IPNLKHLNN-------OTSAIGKFIH 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 TNGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGWATGAFGKTFH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59.5; DB 4; Length 577;
Pred. No. 14;
7; Mismatches 12; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 YYGINGVHCTKNSL---WGKVRLKNMKYDQNTTYMGRLQDILLGWATG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----Trci--INNGAMAWATG 54
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Best Local Similarity 37.5%; Pred. No. 0.99;
Matches 18; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4928, Application US/09543681A
; Patent No. 6607109;
; GENERAL INFORMATION;
; APPLICANT: CARY BRETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 71, Application US/08924629C
Patent No. 6403082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stiles, Michael E. APPLICANT: Vederas, John C. APPLICANT: van Bellvum, Marius J. APPLICANT: Worobo, Randy W. APPLICANT: Worobo, Rodney J. APPLICANT: McMullen, Lynn M. APPLICANT: Leisner, Jorgen J. APPLICANT: Poon, Alsion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 YYG-NGVTCGKHSCSVDWGKA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.6%;
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT Candida albicans US-09-248-796A-18807
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Best Local Similarity
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US-09-543-681A-4928
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US-08-924-629C-71
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US-08-924-629C-7
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US-09-612-575-43
US-09-612-575-43

US-09-612-575-43

Sequence 43, Application US/09632575

Patent No. 6635465

GENERAL INFORMATION:

APPLICANT: Gualfetti, Peter

APPLICANT: Mitchinson, Colin

APPLICANT: Modelfetti, Peter

APPLICANT: Modelfetti, Peter

TITLE OF INVENTION: Mutant EGIII Compositions and Methods for Obtaining Same

TITLE OF INVENTION: Mutant EGIII Compositions and Methods for Obtaining Same

TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same

TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same

TITLE OF INVENTION NUMBER: US/09/632,575

CURRENT APPLICATION NUMBER: US/09/632,575

CURRENT FILING DATE: 2000-08-04

NUMBER OF SEQ ID NOS: 54

SEQ ID NO 43

LENGTH: 244
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                                                                                                                                         Sequence 13, Application US/09632570

Pageuence 13, Application US/09632570

Patent No. 6623949

GENERAL INFORMATION:

APPLICANT: Gualfetti, Peter

APPLICANT: Mitchinson, Colin

APPLICANT: Phillips, Jay Ian

TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase

TITLE OF INVENTION: Compositions

FILE REFERENCE: GC631

CURRENT APPLICATION: 2000-08-04

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
34 TAGAYTIYNNLWGKDNAES--GEQCTINSGEQSDGSIAMSVEWSWTGGGGG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 INGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGWA----TGAFGK 51
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18.3%; Score 55.5; DB 4; Length 244;
Best Local Similarity 31.4%; Pred. No. 17;
Matches 16; Conservative 8; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
18.3%; Score 55.5; DB 4;
Best Local Similarity 31.4%; Pred. No. 17;
Matches 16; Conservative 8; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 70, Application US/08924629C
; Patent No. 6403082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Stiles, Michael E.
APPLICANT: Vederas, John C.
APPLICANT: van Belkum, Marius J.
APPLICANT: Worobo, Randy W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Fusarium javanicum (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Fusarium javanicum (1)
US-09-632-570-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-08-924-629C-70
                                                                                                                                 JS-09-632-570-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-632-575-43
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Sequence 3159, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

TITLE OF INVENTION: BEDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/054,964

PRIOR APPLICATION NUMBER: US 60/054,964

PRIOR PILING DATE: 1997-108-14

PRIOR PILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3159

LENGTH: 10182
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Sequence 13, Application US/09216295
Sequence 13, Application US/09216295
Sequence 13, Application US/09216295
GENERAL INFORMATION:
APPLICANT: Witchinson, Colin
APPLICANT: Wendt, Dan J.
APPLICANT: Wendt, Dan J.
TITLE OF INVENTION: NO. 6268328el Variant EGIII-Like Cellulase Compositions
FILE REFERENCE: GC555
CURRENT APPLICATION NUMBER: US/09/216,295
CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 243
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                                                                                                                                                                                                                                     Query Match 18.4%; Score 56; DB 4; Length 66; Best Local Similarity 60.0%; Pred. No. 2.7; Matches 12; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55.5; DB 3; Length 2
Pred. No. 16;
8; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56; DB 3; I
Pred. No. 1.5e+03;
2; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4753 TORVNTTKNDLNGNDKLAEAKRDANTTIDG 4782
                                                                                         ) NAME/KEY: misc_feature

) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

US-09-107-532A-4680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 TNGVHCTKNSLWGKVRLKNMKYDQNTTYMG 35
                             ORIGINAL SOURCE: ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3159
                                                                                                                                                                                                                                                                                                                                           3 YYGTNGVHCTKNSL---WGK 19
                                                                                                                                                                                                                                                                                                                                                                         26 YYG-NGVYCTKNKCTVDWAK 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Fusarium javanicum (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 46.7%;
Matches 14; Conservative
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Best Local Similarity 31.4%;
Matches 16; Conservative
  HYPOTHETICAL: YES
                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-216-295-13
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6 TNGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGWA-----TGAFGK 51

3

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APPLICANT: Worobo, Rodney J.
APPLICANT: Greer, G. Gordon
APPLICANT: Greer, G. Gordon
APPLICANT: Greer, Joyn M.
APPLICANT: Leisner, Joyn M.
APPLICANT: Leisner, Joyn M.
APPLICANT: Prant, Charles M.A.P.
TITLE OF INVENTION: No. 64030928bacteriocins, Transport and Vector System and Method
FILE REPERENCE: 660.0005US
CURRENT FILING DATE: 1997-09-05
CURRENT APPLICATION NUMBER: US/08/224,629C
CURRENT APPLICATION NUMBER: US/08/224,629C
CURRENT APPLICATION NUMBER: US/08/224,629C
PRIOR FILING DATE: 1996-09-05
SOFTWARE: PRECEDING: 80
SOFTWAR
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OM protein - protein search, using sw model

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(without alignments) 134.618 Million cell updates/sec

US-10-644-927-1

304 1 KTYYGTNGVHCTKNSLWGKV......GRLQDILLGWATGAFGKTFH 54 Perfect score:

Sequence:

Scoring table:

1432185 segs, 334051727 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

'Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications_AA:

/ cgnz 6 prodate 1 pubpaa (1809 PubcoMB. pep: 4 cgn2 6 prodate 1 pubpaa (1809 PubcoMB. pep: 4 cgn2 6 prodate 1 pubpaa (1809 PubcoMB. pep: 4 cgn2 6 prodate 1 pubpaa (1809 Pub CoMB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 PubcoMB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 PubcoMB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 PubcoMB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 PubcoMB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 PubcoMB. pep: 4 cgn2 6 prodate 1 pubpaa (1811 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpaa (1811 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpaa (1811 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpaa (1811 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpaa (1810 NEW PUB. pep: 4 cgn2 6 prodate 1 pubpa (1810 NEW PUB. pe /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.	Score	Match	Match Length DB ID	DB	ID	Description
	09	19.7	36	101		Sequence 69, Appl
7	9	19.7	37	σ	US-09-030-619-209	Sequence 209, App
m	9	19.7	37	6	US-09-912-609-97	Sequence 97, Appl
4	9	19.7	37	15	US-10-277-232-209	Sequence 209, App
ស	9	19.7	37	15	US-10-277-233-209	Sequence 209, App
ø	9	19.7	61	10	US-09-883-343A-68	Sequence 68, Appl
7	09	19.7	300	σ	US-09-982-616-9	Sequence 9, Appli
80	9	19.7	300	10	US-09-773-307B-2	Sequence 2, Appli
σ	9	19.7	300	15	US-10-295-027-1348	Sequence 1348, Ap
10	9	19.7	300	15	US-10-454-238-2	Sequence 2, Appli
11	9	19.7	300	16	US-10-322-696-162	Sequence 162, App
12	9	19.7	300	17	US-10-753-267-34	Sequence 34, Appl
13	59	19.4	62	10	US-09-883-343A-71	Sequence 71, Appl

Sequence 6141, Ap	Seguence 280304,	Sequence	Sequence	Sequence	Sequence	Sequence												Sequence 103806,													
US-10-369-493-6141	0	US-10-424-599-213009	US-10-410-432-10	US-10-669-174-10	US-10-424-599-197752	US-10-282-122A-72532	US-10-424-599-225665	US-09-982-616-11	US-10-282-122A-70580	US-10-661-809-23	US-10-441-626-13	US-10-441-625-13	US-10-425-114-70314	US-10-425-114-60740	US-09-883-343A-70	US-09-738-626-5582	US-10-282-122A-55991	US-10-437-963-103806	US-09-071-035-456	US-10-206-576-456	US-10-912-362-456	US-09-071-035-450	US-09-071-035-454	US-10-206-576-450	US-10-206-576-454	US-10-282-122A-56879	US-10-912-362-450	US-10-912-362-454	US-09-815-242-10936	US-10-838-289-732	L1 US-09-834-309-3
15	15							σ		16						σ	15	16	σ	14	17	σ	0	14	14	15	17	11	σ	17	11
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14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

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APPLICANT: Vederas, Jountal B.
APPLICANT: Vederas, Jountal J.
APPLICANT: Vederas, Jountal J.
APPLICANT: Vederas, Mandy W.
APPLICANT: Worobo, Randy W.
APPLICANT: Worobo, Randy W.
APPLICANT: Worobo, Rodney J.
APPLICANT: Worobo, Rodney J.
APPLICANT: Descr. G. Gordon
APPLICANT: Descr. G. Gordon
APPLICANT: Descr. Charles M.A.P.
APPLICANT: Poon, Alsion
APPLICANT: Poon, Alsion
APPLICANT: Poon, Alsion
APPLICANT: Poon, Misson
APPLICANT: Poon, Alsion
APPLICANT: Poon, Alsion
APPLICANT: Poon, Alsion
APPLICANT: Poon, Alsion
APPLICANT: Boon, Alsion
APPLICANT: WINDER: US/09/883,343A
CURRENT APPLICATION NUMBER: US/08/924,629
PRIOR APPLICATION NUMBER: US/08/924,629
PRIOR PILING DATE: 1997-09-05
PRIOR PILING DATE: 1996-09-05
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 69
LENGTH: 36
                                                          Sequence 69, Application US/09883343A Publication No. US20030039632A1 GENERAL INFORMATION: APPLICANT: Stiles, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mesenteriocin Y105
RESULT 1
US-09-883-343A-69
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3 YYGTNGVHCTKNSL---WGKV-----RLKN 24

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Query Match
19.7%; Score 60; DB 10; Length 36;
Best Local Similarity 48.4%; Pred. No. 2.3;
Matches 15; Conservative 2; Mismatches 4; Indels

US-09-883-343A-69

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Gaps

Indels 10;

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Sequence 209, Application US/10277232 Publication No. US20030211537A1 GENERAL INFORMATION:
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; Sequence 68, Application US/09883343A
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                                                                                                                                                                                                                                                                                                    APPLICANT: Krieger, Timothy J.
APPLICANT: Krieger, Tobert
APPLICANT: Erfle, Douglae
APPLICANT: Erfle, Douglae
APPLICANT: Erfle, Douglae
APPLICANT: Frager, Janet R.
APPLICANT: Frager, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael
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| Publication No. US20020041898A1
| CABREAL INFORMATION:
| APPLICANT: WARSUNAGA, TERRY ONICHI
| APPLICANT: WARASWANI, VARADARAJAN
| APPLICANT: RAMASWANI, VARADARAJAN
| APPLICANT: RAMASWANI, WAREN JOHNER JOHNERY SYSTEMS FOR BIOACTIVE AGENTS
| TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
| TITLE OF INVENTION: NUMBER: US/09/912,609
| CURRENT FILING DATE: 2000-001-25
| PRIOR PAPLICATION NUMBER: US/703,474
| PRIOR FILING DATE: 2000-01-03
| PRIOR FILING DATE: 2000-01-05
| NUMBER OF SEQ ID NOS: 131
| SOFTWARE: PATENTIN VEY: 2.1
| SOFTWARE: PATENTIN VEY: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 37;
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Pred. No. 2.4;
2; Mismatches 4
2 YYG-NGVHCTKSGCSVNWGEAASAGIHRLAN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 YYGTNGVHCTKNSL---WGKV-----RLKN 24
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                                                                                                                                                                                                                     Sequence 209, Application US/09030619B Patent No. US20020035061A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT , ORGANISM: Leuconostoc gelidum US-09-030-619-209
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 48.4%;
Matches 15; Conservative
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Matches 15; Conserva
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APPLICANT: Taylor, Robert
APPLICANT: Target
APPLICANT: Freser, Janet R.
APPLICANT: Wichael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: Monicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
CURRENT APPLICATION WHERE: 2002-11-27
NUMBER OF SEQ ID NOS: 232
SOUTHARD FILING DATE: 2002-11-27
SOUTHARD FILING DATE: 2002-11-27
SEQ ID NO 209
LENGTH: 37
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Sequence 209, Application US/2032750A1

Sequence 209, Application No. US20030232750A1

GENERAL INFORMATION:

APPLICANT: Krieger, Timothy J.

APPLICANT: Erfle, Douglas

APPLICANT: Erfle, Douglas

APPLICANT: Michael H.P.

APPLICANT: Monicol, Patricia J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

TITLE OF INVENTION: WITH ANTIBIOTICS

CURRENT APPLICATION NUMBER: US/10/277,233

CURRENT FILING DATE: 2002-10-18

NUMBER OF SEQ ID NOS: 232

SOFTWARE: FESTEREMENT

LENTHER DATE: DATE: DATE: 2002-10-18

LENTHER DATE: 2002-10-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
19.7%; Score 60; DB:
Best Local Similarity 48.4%; Pred. No. 2.4;
Matches 15; Conservative 2; Mismatches
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19.7%; Score 60; DB
Best Local Similarity 48.4%; Pred. No. 2.4;
Matches 15; Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Leuconostoc gelidum
US-10-277-232-209
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US-10-277-233-209
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TITLE OF INVENTION: Method of Detecting Risk Factor for Onset of Diabetes FILE REPERENCE: PBM37
CURRENT APPLICATION NUMBER: US/09/773,307B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
ERQ ID NO 2
LENGTH: 300
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PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR PELING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PELING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR PILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR PELING DATE: 2002-01-10
PRIOR PELING DATE: 2002-01-10
PRIOR PELING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR APPLICATION NUMBER: US 60/347,314
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR PELING DATE: 2002-02-08
PRIOR PELING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-10
PRIOR FILING DATE: 2002-02-13
PRIOR FILING DATE: 2002-02-13
PRIOR FILING DATE: 2002-02-13
PRIOR FILING DATE: 2002-02-13
PRIOR PILING DATE: 2002-02-13
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TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REPERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
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                                                                                                                                                                                                                                                                                                                                       Length 300;
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                                                                                                                                                                                                                                                                                                                                 Score 60; DB 10;
Pred. No. 25;
7; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1348, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Wark, Nathard
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
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35.0%;
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35.0%;
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Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-10-295-027-1348
                                                                                                                                                                                                                         TYPE: PRT

CORGANISM: Hominidae
US-09-773-307B-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                            APPLICANT: Franz, Charles M.A.P.
TITLE OF INVENTION: No. US20030039632AlelBacteriocins, Transport and Vector System an FILE REPERBURGS: 660.0005US
CURRENT APPLICATION UMBER: US/09/883,343A
CURRENT FILING DATE: 2001-06-19
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Pred. No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
19.7%; Score 60; DB 9; Length 300
Best Local Similarity 35.0%; Pred. No. 25;
Matches 14; Conservative 7; Mismatches 19; Indels
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APPLICANT: Santiago Partida-Sanchez
TITLE OF INVENTION: CD38 MODILATED CHEMOTAXIS
FILE REFERENCE: AP13438 068443.0106
CURRENT APPLICATION NUMBER: US/09/982,616
CURRENT FILING DATE: 2001-10-17
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PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1996-09-05
NUMBER OF SEQ ID NOS: 80
SOFWARE: Patentin version 3.1
LENGTH: 61
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*PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
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                                  Stiles, Michael E.
Vederas, John C.
van Belkum, Marius J.
Worobo, Rodney W.
Worobo, Rodney W.
Greer, G. Gordon
McMullen, Lynn M.
Leisner, Jorgen J.
Poon, Alsion
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Publication No. US20020127646A1
GENERAL INFORMATION:
APPLICANT: France E. Lund
US20030039632A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 19.7
Best Local Similarity 48.4
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-982-616-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Leucocin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-883-343A-68
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US-09-773-307B-2
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LENGTH: 300
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5 GINGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGW
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Best Local Similarity 35.0%; Pred. No. 25;
Matches 14; Conservative 7; Mismatches 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 71, Application US/09883343A Publication No. US20030039632A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-883-343A-71
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                                                                                                                                                                                     Sequence 2, Application US/10454238

Publication No. US20040081981A1

SEQUENCE 2. Application US/10454238

Publication No. US20040081981A1

SERVERAL INFORMATION:

APPLICANT: Equashiro et al.

TITLE OF INVENTION: MCHOO of Detecting Risk Factor for Onset of Diabetes
FILE REPRENCE: MSHIMG.ODIDU1

CURRENT FILING DATE: 2003-06-04

PRIOR APPLICATION NUMBER: US 09/773,307

PRIOR PILING DATE: 2001-01-31

"PRIOR PILING DATE: 2001-01-31

"NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-322-696-162

Sequence 162, Application US/10322696

Publication No. US20040166490A1

GENERAL INFORMATION:
APPLICANT: Malandro., Marc.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 52945201200
CURRENT APPLICATION NUMBER: US/10/322,696

CURRENT FILING DATE: 2003-10-17

NUMBER OF SEQ 1D NOS: 186

SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 19.7%; Score 60; DB 16; Length 30 Best Local Similarity 35.0%; Pred. No. 25; Matches 14; Conservative 7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.7%; Score 60; DB 15; Length 30
35.0%; Pred. No. 25;
tive 7; Mismatches 19; Indels
19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GINGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGW 44
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                                          S GINGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGW
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US-10-753-267-34

is Sequence 34, Application US/10753267

is Publication No. US20050037946A1

ig GENERAL INFORMATION:

is APPLICANT: Millennium Pharmaceuticals, Inc.

is APPLICANT: Stagliano, Nancy E.

is APPLICANT: Healy, Aileen

is APPLICANT: Acton, Susan L.
  7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
  14; Conservative
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ORGANISM: Homo sapiens
US-10-322-696-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEO ID NO 2
LENGTH: 300
TYPE: PRT
ORGANISM: Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 162
LENGTH: 300
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  Matches
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APPLICANT: Stiles, Michael E.
APPLICANT: Vederas, John C.
APPLICANT: Vederas, John C.
APPLICANT: Vederas, John C.
APPLICANT: Worobo, Randy W.
APPLICANT: Worobo, Rodney J.
APPLICANT: Greer, G. Gordon
APPLICANT: McMullen, Lynn M.
APPLICANT: McMullen, Lynn M.
APPLICANT: Poon, Alsion
APPLICANT: Poon, Alsion
APPLICANT: Franz, Charles M.A.P.
TITLE OF INVENTION: No. US20030039632AlelBacteriocins, Transport and Vector System and PILE REFERENCE: 660.0005US
APPLICANT: Donoghue, Mary A. Amelie
APPLICANT: Donoghue, Mary A. Amelie
APPLICANT: Donoghue, Mary A. Amelie
APPLICANT: Tomlingon, James B.
TITLE OF INVENTION: METADON AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: MARCHAEL
TITLE OF INVENTION: 10633, 9215, 21668, 17724, 2210, 6169, 1010.2 21061, 1762, 1711.0 CF INVENTION: 10633, 9215, 21668, 17724, 2210, 6169, 1010.2 21061, 21476, 13710, 1711.0 CF INVENTION: 10633, 9215, 21266, 1729, 65522, 1261, 21476, 13710, 1711.0 CF INVENTION: 1063, 2122, 2525, 4217, 19319, 43669, 9921, 8993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 6993, 9921, 69
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Sequence 280304, Application US/10424599

Sequence 280304, Application US/204031072A1

Sequence 280304, Application US/204031072A1

Publication No. US20040031072A1

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steegory J.
APPLICANT: Slater, Steeyen C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 ($2.05.2)
FURRENT APPLICATION NUMBER: US/10/369,493
FURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                20 YYG-NGVTCGKHSCSVDWGKA-----TTCI--INNGAMAWAIG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Query Match 19.4%; Score 59; DB 15; Length 399; Best Local Similarity 35.8%; Pred. No. 47; Matches 19; Conservative 4; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                DB 10; Length 62;
                                                                                                                                                                                                                                                                                                           Query Match
19.4%; Score 59; DB 1
Best Local Similarity 37.5%; Pred. No. 5.8;
Matches 18; Conservative 5; Mismatches
PRIOR APPLICATION NUMBER: US/08/924,629
PRIOR FILING DATE: 1997-09-05
PRIOR PAPLICATION NUMBER: US 60/026,257
PRIOR FILING DATE: 1996-09-05
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SEQ ID NO 71
LENGTH: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 6141, Application US/10369493; Publication No. US20030233675A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6141
                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pediocin PA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-369-493-6141
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LENGTH: 95
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LENGTH: 399
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 16, 2005, 17:25:23 ; Search time 39 Seconds (without alignments) 133.223 Million cell updates/sec Run on:

Title: Perfect score:

US-10-644-927-1 304 1 KTYYGTNGVHCTKNSLWGKV......GRLQDILLGWATGAFGKTFH 54 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		glutamate-ammonia	hypothetical prote		hypothetical prote	glutamate-ammonia	leucocin A-UAL 187	mesentericin Y105	lymphocyte surface	spermidine synthas	pediocin PA-1 prec	hypothetical prote		inositol-3-phospha	gene 12 protein -	hepatocyte growth	parasporal crystal	PBSX prophage ORF	31K outer-membrane	aminomethyltransfe	hypothetical prote	probable nucleosid	nerve growth facto	hypothetical prote	phosphate starvati	glycosyltransferas	hypothetical prote	1-aminocyclopropan	tail fiber protein	hypothetical prote
SUMMARIES	TD CI		S11899	A99180	838508	AF2555	A43995	A41657	S52208	A43521	F84954	A48941	T20455	T18995	T50021	GIBPT4	PC2131	B29838	F69732	AD3302	B90243	T24205	G84442	TVRTTB	T15463	D86760	F97257	B96806	B41141	TLBPM1	S51815
	DB	1	N	~		~	~	7	~	~	~	Н	8	7	7	-	7	~	~	7	~	7	~	-	7	~	N	~	-	Н	7
	Length		471	471	61	290	446	61	61	300	286	62	399	3036	510	517	132	934	1332	201	346	369	516	799	319	322	374	383	494	262	269
	Query			1.5	1.1	0.7	9.0	7.6	7.6	.7	9.6	4.	4.	7.	6.	9.8		<u>س</u>	8.3	3.1	7.	7.	8.1		7.9	7.9	٠	7.9	7.9	7.8	7.8
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	Score		65.5	65.5	64	63	62.5	09	9	9	59.5	59	59	58	57.5	56.5			55.5	55	55	55	55	55				54.5	54.5	54	54
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<pre>sodium/proline sym chlorophyll a/b-bi transcription requ</pre>	threonine-tRNA lig probable myo-inosi gene 12 protein -	complement UsarAeps hypothetical prote phage related prot FUN81 protein - ye	hypothetical prote probable EtfB2 ele tail fiber adhesin	cellulase (BC 3.2. glutathione transf TOM37 protein - ye
JC2382 S31393 G69515	YSBYTM D84610 S29530	FL0009 H71609 B69948 S49628	C90228 B95357 T13591	JU0328 AI3308 S54560
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494 324	510 510 527	1166 1166 1585 167	202 249 258	264 327 327
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30 31 32	. W W W V	3 3 3 4 8 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 4 4 4 4 2 4 2 4 2 4 4 4 4 4 4 4 4	4 4 4 6 4 3

ALIGNMENTS

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Glutamate-ammonia ligase (EC 6.3.1.2) - Sulfolobus solfataricus
Glutamate names: glutamine synthetase
C; Species: Sulfolobus solfataricus
C; Date: 19.97 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C; Date: 19.97 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C; Accession: S11899
R; Sanangelantoni, A.M.; Barbarini, D; di Pasquale, G; Cammarano, P.; Tiboni, O.
Mol. Genet. 221, 187-194, 1990
A; Title: Cloning and nuclocide sequence of an archaebacterial glutamine synthetase gene A; Reference number: S11899
A; Millson Mullson M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
21.5%; Score 65.5; DB 2; Length 471;
Best Local Similarity 48.6%; Pred. No. 1.8;
Matches 17; Conservative 2; Mismatches 13; Indels
RESULT 1
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1 KTYYGTN--GVHCTKNSLWGKVRLKNMKYDQNTTY

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5

Gaps

3,

33

288 255 KPIYGDNGTGMH-THLSLWTKDGKKNLMYDPNDEY 셤

hypothetical protein glnA-1 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: A99180
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139

A;Accession: A99180
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-471 cKOR>
A;Cross-references: UNIPROT:P23794; GB:AE006641; NID:g13813510; PIDN:AAK40696.1; GSPDB:G:
C;Genetics:
A;Gene: glnA:
C;Superfamily: glutamate-ammonia ligase

3; Gaps Query Match

21.5%; Score 65.5; DB 2; Length 471;
Best Local Similarity 48.6%; Pred. No. 1.8;
Matches 17; Conservative 2; Mismatches 13; Indels 3

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26 YYG-NGVHCTKSGCSVNWGEAFSAGVHRLAN 55
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 35.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-446 <POS>
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A;Residues: 1-61 <HAS>
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A;Residues: 1-590
                                                                                                                                              A;Gene: all8037
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
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A; Accessions is 25/11.

A; Rocessions is 25/11.

A; Rocessions is 25/11.

A; Cross-references: UNPROT: P35618; EMBL: Z48542; NID: 9695615; PIDN: CAA88428.1; PID: 96956

A; Experimental source: strain lb674

R; H04Ck, A.L.; Axelsson, L.; Huehne, K.; Kroeckel, L.

FEMS Microbiol. Lett. 115, 143-150, 1994

A; Title: Purification and cloning of sakacin 674, a bacteriocin from Lactobacillus sake
A; Reference number: S57915; MUID: 94186010; PMID: 8138128

A; Reference number: S57915; MUID: 94186010; PMID: 8138128

A; Residues: EMBL: Z25816; NID: 9414124; PIDN: CAA81064.1; PID: 9414125

A; Cross-references: EMBL: Z25816; NID: 9414124; PIDN: CAA81064.1; PID: 9414125

A; Cross-references: EMBL: Z35816; NID: 9418124; PIDN: CAA81064.1; PID: 9414125

A; Cross-references: EMBL: Z35816; NID: 94236240; PMID: 9180701

A; Residues: 1-61 kTIC

A; Residues: 1-61 kTIC

A; Residues: 1-61 kTIC

A; Cross-references: EMBL: X75081; NID: 9475950; PIDN: CAA52974.1; PID: 9475952

C; Genetics:
A; Genetics:
A; Genetics:
C; Keywords: antibacterial; bactericoin
C; Keywords: a
                                                                                                                                                                                                                                                            S38508
sakacin P precursor - Lactobacillus sake (strains Lb674 and LTH673)
C;Species: Lactobacillus sake
A;Variety: strains Lb 674 and LTH 673
A;Variety: strains Lb 674 and LTH 673
C;Date: 25-Dec-1994 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S57911; S57915; S31869; S38604
B;Huchne, K.; Holck, A.; Axelsson, L.; Kroeckel, L.
submitted to the EMBL Data Library, February 1995
A;Abscription: Purification and cloning of sakacin 674, a bacteriocin from Lactobacillus
A;Accession: S57911
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AP82555
hypothetical protein all8037 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120ga
hypothetical protein all8037 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120ga
S.Note: Nostoc sp. Errain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C.Accession: AF2555
R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4,
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Pred. No. 0.28;
4; Mismatches 9; Indels
                                                                                                         255 KPIYGDNGTGMH-THLSLWTKDGKKNLMYDPNDEY 288
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36.7%;
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Matches 18; Conservative
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A;Cross-references: UNIPROT:Q8YK80; GB:AP003603; PIDN:BAB77367.1; PID:g17134810; GSPDB:G1
A;Experimental source: strain PCC 7120
C;Genetics:
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C;Species: Leuconostoc gelidum
C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 09-Jul-2004
C;Accession: A41657
Bacteriol. 173, 7491-7500, 1991
A;Title: Characterization of leucocin A-UAL 187 and cloning of the bacteriocin gene from A;Reference number: A41657; MUID:92041660; PMID:1840587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P34034; GB:M64371; NID:g149637; PIDN:AAA68003.1; PID:g149638
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 09-Jul-2004
C;Accession: A43995; S13504
R;Possot, O.; Sibold, L.; Aubert, J.P.
R;Possot, O.; Sibold, L.; Aubert, J.P.
A;Title: Nucleotide sequence and expression of the glutamine synthetase structural gene, A;Reference number: A43995; MUID:90139872; PMID:2575777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT: P21154; GB: X53509; NID: 944711; PIDN: CAA37585.1; PID: 944712
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                                                                                                                                                                                                                        Gape
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                                                                                                                                                                                                                                                                           3 YYGINGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGWATGAFGKTF
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                                                                                                                                                                        DB 2; Length 590;
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                                                                                                                                                                                                                        23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    glutamate-ammonia ligase (BC 6.3.1.2) - Methanococcus voltae N'Alternate names: glutamine synthetase C;Species: Methanococcus voltae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
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                                                                                                                                                                   Score 63; DB 2;
Pred. No. 5;
8; Mismatches
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Pred. No. 4.2;
9; Mismatches
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19.7%; Score 60;
Best Local Similarity 48.4%; Pred. No. (
Matches 15; Conservative 2; Mismatch
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C;Superfamily: carnobacteriocin precursor
C;Keywords: bacteriocin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: glnA
C,Superfamily: glutamate-ammonia ligase
C,Keywords: ligase
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20.6%;
Best Local Similarity 33.9%;
Matches 19; Conservative
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pediocin PA-1 precursor - Pediococcus acidilactici plasmid pSRQ11
C;Species: Pediococcus acidilactici
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48941; S21699; A47680; A41018; A41823
R;Marugg, J.D.; Gonzalez, C.F.; Kunka, B.S.; Ledeboer, A.M.; Pucci, M.J.; Toonen, M.Y.; FAPPPL: Environ. Microbiol. 58, 2360-2367, 1992
A;Title: Cloning, expression, and nuclectide sequence of genes involved in production of A;Reference number: A48941; MUID:92384551; PMID:1514784
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A;Experimental source: strain PAC1.0, plasmid pSRQ11
A;Note: sequence extracted from NCB1 backbone (NCBIN:112082, NCBIP:112083)
R;Handerson, J.T.; Chopko, A.L.; van Wassenaar, P.D.
A;Ch. Biochem. Biophys. 295, 5-12, 1992
A;Title: Purification and primary structure of pediocin PA-1 produced by Pediococcus acic
A;Reference number: S21699; MUID:92246549; PMID:1575516
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A,Molecule type: protein
A,Residues: 19-62 <HEN>
R,Residues: 19-62 <HEN>
A,Residues: 19-62 (HEN>
A,Ricto Lozano, J.C.; Meyer, J.N.; Sletten, K.; Pelaz, C.; Nes, I.F.
A,Gen. Microbiol. 138, 1985-1990, 1992
A,Title: Purification and amino acid sequence of a bacteriocin produced by Pediococcus ac A,Reference number: A47680; MUID:93019000; PMID:1402795
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Reference number: A84930; MUID:20445173; PMID:10993077
                                                                                                                                                                       C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
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                                                                                                                         spermidine synthase (EC 2.5.1.16) [imported] - Buchnera sp. (strain APS)
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                                                                                                                                                                                                                                                                   C;Accession: P84954
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa,
Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.6%; Score 59.5; DB 2; Length 286; ilarity 42.1%; Pred. No. 6.2; Conservative 4; Mismatches 9; Indels 5
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C;Keywords: antibacterial; bacteriocin
F;1-18/Domain: propeptide #status predicted <PRO>
F:19-62/Product: pediocin PA-1 #status experimental
F;27-32,42-62/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPDB:GN00144
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Les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: Pry-C;Keywords: transferase
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A; Residues: 1-62 < MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                  A; Genering Control of Mesentericin Xios genetic determinats.

A; Genering Control of Mesentericin Xios genetic determinats.

A; Accession: $52204

A; Accession: $52204

A; Accession: $52208

A; Genering Control of Mesentericin Xios, PIDN:CAAS7405.1; PID:g6090

A; Residues: 1-61 < RRE>

A; Cross-references: UNIPROT:P38577; EMBL:X81803; NID:g609082; PIDN:CAAS7405.1; PID:g6090

A; Residues: 1-61 < RRE>

A; Cross-references: UNIPROT:P38577; EMBL:X81803; NID:g609082; PIDN:CAAS7405.1; PID:g6090

A; Title: Characterization and purification of mesentericin Yios, an anti-Listeria bacter

A; Reference number: A47690; MUID:93139768; PMID:1487737

A; Reference number: A47690; MUID:93139768; PMID:1487737

A; Reference number: A47690; MUID:93139768; PMID:1487737

A; Reference number: A560 < RES

A; Residues: Breliminary

A; Residues: Breliminary

A; Residues: Boctein

C; Reywords: bacteriocin
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C;Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 09-Jul-2004
C;Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 09-Jul-2004
C;Accession: A3221
R;Jackson, D.G.; Bell, J.I.
J. Immunol. 144, 2811-2815, 1990
A;Title: Isolation of a cDNA encoding the human CD38 (T10) molecule, a cell surface glych A;Reference number: A43521; MUID:90203621; PMID:2319135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :Molecule type: mRNA
;Residues: 1-300 <JAC>
:Cross-references: UNIPROT:P28907; GB:M34461; NID:g862620; PIDN:AAA68482.1; PID:g180119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternate names: ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase; OKT10 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 4p15-4p15
C;Superfamily: ADP-ribosyl cyclase CD38
C;Superfamily: ADP-ribosyl cyclase CD38
C;Superfamily: ADP-ribosyl cyclase CD38
C;Supervals: B-cell; glycoprotein; surface antigen; T-cell; transmembrane protein F;1-21/Domain: intracellular #status predicted <CYT>
F;22-44/Domain: transmembrane #status predicted <TWM>
F;45-300/Domain: extracellular #status predicted <EXT>
F;100,164,209,219/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۳
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S52208
mesentericin Y105 - Leuconostoc mesenteroides
CSpecies: Andrew March Ma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GINGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGW 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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Pred. No. 0.92;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 YYG-NGVHCTKSGCSVNWGEAASAGIHRLAN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 YYGTNGVHCTKNSL---WGKV-----RLKN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lymphocyte surface glycoprotein CD38 - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.78;
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Matches 15; Conserva
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26 YQTTELVHENKNGAFQM-TVKPKTVKYEFKTDTHVPKLGVMLVGWG-GNNGST
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A;Residues: 1-517 <SBL>
A;Cross-references: BBL:XO6792
A;Note: the authors translated the codon CAG for residue 279 as His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
18.6%; Score 56.5; DB 1; Length 517;
Best Local Similarity 33.3%; Pred. No. 30;
Matches 15; Conservative 8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416 GVGCTGGYV-GEVQIQQMSYHKHAAGGFGEHDDL-----GAFGNT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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18.9%; Score 57.5; D
Best Local Similarity 37.7%; Pred. No. 22;
Matches 20; Conservative 8; Mismatches
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C,Superfamily: phage T4 gene 12 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Accession: PC2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, Genetics:
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18995
R;Steward, C.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19057
A;Accession: T18995
A;Acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:017755; EMBL:281054; PIDN:CAB02882.1; GSPDB:GN00022; CESP:FG C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F01D4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jul-2004
C;Accession: T20455
R;Wild, A.
A;Reference number: Z19278
                                                                                      Gaps
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                                                                                                                                                                    3 YYGINGVHCTKNSL---WGKVRLKNMKYDQNTTYMGRLQDILLGWATG 47
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Pred. No. 1.4e+02;
5; Mismatches 24; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 35.8%; Pred. No. 10;
Matches 19; Conservative 4; Mismatches 22; Indels
                                                                                                                                                                                                                            20 YYG-NGVICGKHSCSVDWGKA-----ITCI--INNGAMAWAIG
Query Match 19.4%; Score 59; DB 1; Length 62; Best Local Similarity 37.5%; Pred. No. 1.3; Matches 18; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 26.1%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:F01D4.3
A;Map position: 4
A;Introns: 45/3; 235/2; 294/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               603 RILNNWGDG 611
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T18995
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T50021
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inositol-3-phosphate synthase (EC 5.5.1.4) T31P16.160 [similarity] - Arabidopsis thalians N.Alternate names: protein T31P16.160 [similarity] - Arabidopsis thaliana (Governate names: protein T31P16.160 [c.Species: Arabidopsis thaliana (Mouse-ear cress) [c.Species: Arabidopsis thaliana (Mouse-ear cress) [c.Species: D5-010-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004 [s.Species: T5001] R.Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Kalicki, J.; Wohldmann, P.; Smisubmitted to the Protein Sequence Database, May 2000 A.Reference number: Z25027 A.Accession: T5001 A.Accession: T5001 A.Accession: T5001 A.Accession: T5001 A.Accession: Database A.Accession: Virginia, M.; Kawano, S.; Teuji, S.; Ito, T.; Hayashi, N.; Horimoto, M.; Mita, E.; Nagand Biochem. Biophys. Res. Commun. 200, 536-541, 1994
A;Title: Increased expression of c-met messenger RNA following acute gastric injury in rs A;Reference number: PC2131; MUID:94220137; PMID:8166728
A;Accession: PC2131
A;Accession: PC2131
A;Accession: PC2131
A;Reference number: PC3131
A;Reference number: PC3131 A;Residues: 1-510 <BEV>
A;Residues: UNIPROT:Q9LX12; EMBL:AL356332; GSPDB:GN00063; ATSP:T31P16.160
A;Experimental source: cultivar Columbia; BAC clone T31P16 bacteriophage T4 gene 12 4 7 gene 12 protein - phage T4
NiAlternate names: tail fiber protein
Cispecies: phage T4
Cispecies: phage T4
Cispecies: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 30-Jun-1993
Cispecession: SO1889
Riselivanov, N.A.; Prilipov, A.G.; Mesyanzhinov, V.V.
Nucleic Acids Res. 16, 2334, 1988
A;Reference number: SO1889; MUID:88189824; PMID:3357780
A;Reference number: SO1889 heparocyte growth factor receptor - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004 Gaps A;Gene: ATSP:T31P16.160
A;Map position: 5
A;Introns: 63/2; 86/2; 131/3; 214/2; 290/1; 328/3; 387/3; 450/3; 471/3
A;Introns: 63/2; 86/2; 131/3; 214/2; 290/1; 328/3; 387/3; 450/3; 471/3
C;Superfamily: myo-inositol-1-phosphate synthase
C;Keywords: intramolecular lyase; isomerase; NAD 25 96 5;

; 7 Query Match 18.3%; Score 55.5; DB 2; Length 132; Best Local Similarity 31.4%; Pred. No. 8.4; Matches 16; Conservative 7; Mismatches 17; Indels 11; Gaps

Search completed: May 16, 2005, 17:34:43 Job time : 41 secs

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Sulfolobus.
NCBI_TaxID=2287;
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08vv63 bacillus th

09pz03 xestia c-ni

08a1j6 bacteroides

07qed anopheles g

09d193 human immun

09d179 human immun
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Q8yk80 anabaena sp
Q8riml fusobacteri
Q8rhh7 fusobacteri
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165.582 Million cell updates/sec
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1 KTYYGTNGVHCTKNSLWGKV......GRLQDILLGWATGAFGKTFH
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O53446
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                        1612378 segs, 512079187 residues
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Q75CA6

SAKP LACSK

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QBIAL9
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
                                                                                                                                   SEQUENCE FROM N.A.
STRANH-ATCC 10895;
Brachat S., Voegeli S.E., Dietrich F.S., Lerch A., Gaffney T.,
Philippsen P.;
                                                                                                                                                                                                                                                                                                                                                                   Score 64.5; DB 2; Length 1071;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                               1071 AA; 123572 MW; 0816B52D60032663 CRC64;
                                                                                                                                                                                                                                  Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases EMBL, AE016816; AAS51233.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 GVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGWATGA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAKP LACSK STANDARD; PRT; 61 AA. P35618; Q57121; 01-JUN-1994 (Rel. 29, Created) 16-QC-2001 (Rel. 40, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Bacteriocin sakacin P precursor (Sakacin 674)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEMS Microbiol. Lett. 115:143-150(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96262715; PubMed=8704983;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
21.2%;
Best Local Similarity 31.7%;
Matches 13; Conservative
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                                                                                 NCBI_TaxID=33169;
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                                                                                                                                                                                                                                                                                            AGD; ACR006C;
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STRAIN-ATC 35092 / DSM 1617 / P2;

MEDLINE-21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Wehher C.C.Y. (Zlausen I.G., Curtis B.A.,

De Moore A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Median N., Peng X.,

Thi-Ngoc H.P., Redder P., Schem M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

-I- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                   "Cloning and nucleotide sequence of an archaebacterial glutamine synthetase gene: phylogenetic implications."; Mol. Gen. Genet. 221:187-194(1990).
                                                                                 Sanangelantoni A.M., Barbarini D., di Pasquale G., Cammarano P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3,
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S -> T (in Ref. 1).

1CC4239287B6C2CD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L-glutamine.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the glutamine synthetase family.
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Last sequence update)
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EMBL; X53263; CAA77352.1; -...
EMBL; ABO06669; AAK40696.1; -...
ETK; A99180; A99180.

PIK; S11899; S11899.

HSSP; P06201.1 LGR.

INTERPRO; IPR00140; Gln Synt Deta.

INTERPRO; IPR00140; Gln Synt C.

PEam; PF00120; Gln-Synt C;

PEam; PF00120; Gln-Synt C;

TIGRFAM9; TIGR00653; Gln Synt C;

TIGRFAM9; TIGR00653; Gln Synt C;

PROSITE; PS00180; GLNA 1;

PROSITE; PS00181; GLNA ATP; 1.
     (1)
SEQUENCE FROM N.A.
MEDLINE=90318316; PubMed=1973523;
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471 AA; 53347 MW;
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
ACROGGE,
ORFNames=ACROOGC;
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Q75CA6;
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Huehne K., Axelsson L., Holck A., Kroeckel L.; "Analysis of the sakacin P gene cluster from Lactobacillus sake Lb674 and its expression in sakacin-negative Lb. sake strains."; Microbiology 142:1437-1448(1996).
                                                                                                                                                                                                               MEDLINE-54236240; PubMed-8180701;
Tichaczek P.S., Vogel R.F., Hammes W.P.;
"Cloning and sequencing of sakp encoding sakacin P, the bacteriocin produced by Lactobacillus sake LTH 673.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of the bacteriocins curvacin A from Lactobacillus curvacus LTH673.";
"Characterization of the bacteriocins curvacin A from Lactobacillus curvacus LTH1174 and sakacin P from L. sake LTH673.";
Syst. Appl. Microbiol. 15:460-465(1992).
I- FUNCTION: Bactericidal activity; inhibits closely related Lactobacilli, Listeria monocytogenes and ivanovvi, Enterococcus faccalis, Carnobacterium sp and Brocothrix thermosphacta.
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARITY: Belongs to the bacteriocin class IIA/YGNGV family.
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94186010; PubMed=8138128; DOI=10.1016/0378-1097(94)90005-1;
                                                                                                                                                                                                                                                                                                                                                                              Holck A.L., Axelsson L., Huehne K., Kroeckel L., Internation and cloning of sakacin 674, a bacteriocin from Lactobacillus sake Lb674.";
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., SEQUENCE OF 19-61, AND CHARACTERIZATION
                                                                            Name=sakP; Synonyms=sakR, sppA;
Lactobacillus sakei.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus
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Matches

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RESULT 3 Q75CA6 ID Q75C AC Q75C DT 05-J DT 05-J DE ACRO GN ORFN

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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEOUENCE 1582 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         NCBI_TaxID=76856;
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                                                                 QBRIM1
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                        RESULT 6
QBRIM1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the between a Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 YIGT--PRGTKFQVVGNKRITNIPEDKNRLYLPDVQRGILVSGSGGSGKTF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 YYGTNGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILLGWATGAFGKTF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 YYG-NGVHCGKHSCTVDWG------TAIGNIGNNAAANWATG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 YYGINGVHCTKNSL---WGKVRLKNMKYDQNTTYMGRL-QDILLGWATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.7%; Score 63; DB 2; Length 590; 35.3%; Pred. No. 21; ive 8; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 64; DB 1; Length 61;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    590 AA; 64933 MW; 7ECA68DF6FE3B469 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
B7BF14DCDD28A73D CRC64;
                                                                                                                                                                                                                                                                                                                        Pfam; PF01721; Bacteriocin II; 1.
ProDom; PD004452; Bacteriocin II; 1.
TIGRFAMB; TIGR01847; bacteriocin sig; 1.
Antibiotic; Bacteriocin; Direct protein sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriocin sakacin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                         InterPro; IPR002633; Bacteriocin_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                      EMBL; X75081; CAA52974.1; -.
EMBL; Z25816; CAA81064.1; -.
EMBL; Z48542; CAA88428.1; -.
EMBL; AF002276; AAB93970.1; -.
PIR; S57911; S38508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         All8037 protein.
OrderedLocusNames=all8037;
Anabaena sp. (strain PCC 7120).
Plasmid pCC7120gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.1%;
36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AA; 6385 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 35.3
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Q8YK80;
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Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan V., Chaga O., Goltsman B., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N.C., Overbeek R.; Genstein M., Kyrpides N.C., Overbeek R.; Genstein Strain ATCC 2586.", J. Bacteriol. 184:2005-2018 (2002).

Binis, Agnide4, Ablasseo.1, E. Emis. Agnide4, Ablasseo.1, InterPro; IPR005546, Auto transpibeta.

InterPro; IPR001014; Ribosomal L23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 YGTNGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILL----GWATGAFGKTF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25566."; J. Bacteriol. 184:2005-2018(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8;
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Pred. No. 62;
6; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                             Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1582 AA; 167889 MW; 666C38783A00EB4F CRC64;
                                                                                                                                          Last sequence update)
Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                         Fusobacterium outer membrane protein family.
PRT; 1582 AA.
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Best Local Similarity 35.2%; Pred. No. 9
Matches 19; Conservative 6; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AE010507, AAL94131.1, -.
InterPro, IPR005546, Auto transptbeta.
Pfam; PF03797, Autotransporter, 1.
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MEDLINE=21886394; PubMed=11889109;
DOI=10.1128/JB.184.7.2005-2018.2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOI=10.1128/JB.184.7.2005-2018.2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
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                                                                          01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                OrderedLocusNames=FN1554;
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Ito T., Sahara K., Bando H., Asano S.; "Cloning and Expression of Novel Crystal Protein Genes cry39A and 39orf2 from Bacillus thuringiensis subsp. alzawai Bunl-14 Encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
VCBI_TaxID=51677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=99434230; PubMed=10502508; DOI=10.1006/viro.1999.9894;
Hayakawa T., Ko R., Okano K., Seong S.I., Goto C., Maeda S.;
"Sequence analysis of the Xestia c-nigrum granulovirus genome.";
Virology 262:277-297(1999).
EMBL; AF162221; AAF05154.1; -,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; MIO.032; --.

GO; GO:0005578; C:extracellular matrix (Bensu Metazoa); IEA.

GO; GO:000422; P:metalloendopeptidase activity; IEA.

GO; GO:0005508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR000585; Hemopexin.

InterPro; IPR001685; Peptidase M.

InterPro; IPR001625; Peptidase M.

InterPro; IPR001625; Pept MIOA_M12B.

InterPro; IPR001635; Pept MIOA_M12B.

SMART; SM00235; ZnMc; 1.
                                                                                                                                                                                                                                                                                                                                                                      20.6%; Score 62.5; DB 2; Length 5 27.7%; Pred. No. 23; tive 8; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 VHCTKNS-----LWGKVR-LKNMKYDQNTTYMGRLQDILLGWAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 IECMSNEHSSKEEMMLWDEVKQAKQLSWSRNLLYNGDFEDVSNGWKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xestia c-nigrum granulosis virus (XnGV) (Xestia c-nigrum
                                                                                                               Bacillus thuringiensis (subsp. aizawai).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                     Mosquitocidal Proteins.",
J. Insect Biotechnol. Sericology 71:123-128(2002).
EMBL; ABO74411; BAB72017.1; -SEQUENCE 558 AA; 63360 MW; 26F6D5A013834207 CRC64;
              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
          01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                          Cry390RF2 protein.
                                                                                                                                                      NCBI_TaxID=1433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=ORF40;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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دي
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 KPFFGMNGSGMHCNQ-SIWLDGKPSF---YDENNAH--QLSDICLSYIGGILEHT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                        1358 FGTNGEYKTDTA--GVIDYKNHAY--GVAYVHENEDIKLGRGIGWYTGIVHNTF 1407
                                                                                                                                                                                                                                                                                                            01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KTYYGTN--GVHCTKNSLW--GKVRLKNMKYDQNTTYMGRLQDILLGWATGAFGKT
                                                                                                                                     4 YGTNGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILL----GWATGAFGKTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 446;
                                                     20.7%; Score 63; DB 2; Length 1630; 35.2%; Pred. No. 64; 11 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-glutamine.
-- SUBCELLULAR LOCATION: Cytoplasmic.
-- SIMILARITY: Belongs to the glutamine synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 62.5; DB 1; Length 44
Pred. No. 18;
9; Mismatches 17; Indels
                172741 MW; 38E9CE42F037B75A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea, Euryarchaeota, Methanococci, Methanococcales, Methanococcaceae, Methanococcus.
NCBI_TaxID=2188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             446 AA; 50199 MW; 95449E4DE8542690 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P06201, 1LGR.
INLERPRO, 1PR008147; Gln synt beta.
INLERPRO, 1PR008146; Gln synt_C.
INLERPRO, 1PR004809; GlnA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00120; Gln-synt_C; 1.
Pfam; PF00351; Gln-synt_N; 1.
ProDom; PD001057; Gln synt_C; 1.
TIGRPAMs; TIGR00653; GlnA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00180; GLNA_1; 1. PROSITE; PS00181; GLNA_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X53509; CAA37585.1; -. PIR; A43995; A43995.
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33.9%;
                                                                        Local Similarity 35.2%;
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                 Methanococcus voltae.
                  1630 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
Nes 19; Conserva
Complete proteome SEQUENCE 1630 A
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P21154;
                                                                                                                                                                                                                                                                                                                                                                                             Name=glnA;
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                                                       Query Match
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GLNA_METVO
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Q8VW63
ID Q8VW
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Gaps

6

46

DB 2; Length 558;

3 6 20.2%; Score 61.5; DB 2; Length 469; 35.9%; Pred. No. 26; tive 9; Mismatches 7; Indele PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1. SEQUENCE 469 AA; 53808 MW; 1BF4EB5C2101E241 CRC64; | : : |:||:|| | ||:||:|| 335 GDDEIIATRNNLW-----YEYHKNSTLMNVGRVQDVL 366 5 GINGVHCTKNSLWGKVRLKNMKYDQNTTYM--GRLQDIL 41

RESULT 11 Q8A1J6

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PRELIMINARY;

QBVW63

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PRELIMINARY;
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                                                                                                                                                                                       STRAINEVPI-5482 / ATCC 29148;
STRAINEVPI-5482 / ATCC 29148;
STRAINEVPI-5482 / ATCC 29148;
MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
Xu J., Bjursell M.K., Himcod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
A genomic view of the human Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003)
EMBL; AB016941; AA078770.1; -.
EMBL; AB016941; AA078770.1; -.
EMBL; AB016975; P:carbohydrate metabolism; IEA.
GO; GO:0004565; P:carbohydrate metabolism; IEA.
FEUR; PF01120; Alpha_L_fucos; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 YYGTNGVHCTKNSLWGKVRLKNMKYDQ-NTTYMGRLQDILLGWATGA-----FGKTFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCP7363 (Fragment).
Names=agCd6405; ORFNames=ENSANGG0000009373;
Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396 TLYGTT----TAATLIGMEQVRHMQYDAFRSF--SLDDILLUGGGTGSF 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TYYGINGVHCTKNSLWGKVRLKNMKYDQNTTYMGRLQDILL-GWATGAF 49
                                                                                                                             Bacteria, Bacteroidetes, Bacteroides (class), Bacteroidales,
Bacteroidaceae, Bacteroides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                             547 AA; 62869 MW; 312E45B01B6C67CB CRC64;
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                 Last sequence update)
Last annotation update)
547 AA
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Best Local Similarity 32.2%; Pred. No. 30;
Matches 19; Conservative 5; Mismatches
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20.2%; Score 61.5; D
Best Local Similarity 38.8%; Pred. No. 32;
Matches 19; Conservative 9; Mismatches
                                  Created)
PRT;
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EMBL, AAABO1008847; EAA06870.1; -. InterPro; IPR004878; DUF270.

Pfam; PF03189; DUF270; 1.

NON_TER
                                                                                                                Bacteroides thetaiotaomicron.
                            (TrEMBLrel. 24, C (TrEMBLrel. 24, I (TrEMBLrel. 25, I
                                                                               Alpha-L-fucosidase.
OrderedLocusNames=BT3665;
 PRELIMINARY:
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SEQUENCE 547 AA
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                                                                                                                                                            NCBI_TaxID=818;
                              01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7QED6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
Q7QED6
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Greenberg M.L.;
"Evolution of the human immunodeficiency virus type 1 envelope during infection reveals molecular corollaries of specificity for coreceptor utilization and AIDS pathogenesis.";
J. Virol. 74:11858-11872(2000).
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                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=20541986; PubMed=11090186;
DOI=10.1128/JVI.74.24.11858-11872.2000;
Hu, Qx, Barry A.P., Wang, Zx, Connolly S.M., Peiper S.C.,
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DOI=10.1128/JVI.74.24.11858-11872.2000;
Hu, Qx, Barry A.P., Wang, Zx, Connolly S.M., Peiper S.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hu Q.-X., Barry A.P., wany a...,
Peiper S.C., Greenberg M.L.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF310113, AAG36991.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                853 AA; 96901 MW; 4BB4C83101B632E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR0000328; Env GP41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 NGVHCTKNSLWGKVR---LKNMKYDQNTTYMGRLQDILL 42
                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                          Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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853 AA.
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PRT;
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01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2003 (TrEMBLrel. 24,
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Matches 14; Conservative
                                                                                                        Envelope glycoprotein.
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SEQUENCE FROM N.A.
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Search completed: May 16, 2005, 17:34:00 Job time : 170 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sailer M., Helms G.L., Henkel T., Niemczura W.P., Stiles M.E., Vederas J.C.;
Vederas J.C.;
115N- and 13C-labeled media from Anabaena sp. for universal isotopic
labeling of bacteriocins: NMR resonance assignments of leucocin A from
Leuconostoc gelidum and nisin A from Lactococcus lactis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98060758; PubMed=9398233; DOI=10.1021/bi971263h; Gallagher N.L.F., Sailer M., Niemczura W.P., Nakashima T.T., Stiles M.E., Vederas J.C.; Tructure of leucocin A in trifluoroethanol and dodecylphosphocholine micelles: spatial location of residues critical for biological activity in type IIa bacteriocins from lactic acid
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Bacteriocin leucocin A precursor (Leucocin A-UAL 187) (Leu A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92041660; PubMed=1840587;
Hastings J.W., Sailer M., Johnson K., Roy K.L., Vederas J.C.,
Stiles M.E.;
Hu Q.-X., Barry A.P., Wang Z.-X., Connolly S.M., Goodman D., Peiper S.C., Greenberg M.L.; Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF310128; AAG37006.1; -- HSSP; P04578; 1DLB.
                                                                                                                                                                                                                                 Length 858;
                                                                                                                                                                                                                                                        14; Indels
                                                                                                                                                                                                       858 AA; 97622 MW; B3D64720CF57DF4F CRC64;
                                                                                                                                                                                                                                                                                                136 || | | :|:|: | : : | :: | :: | 174
                                                            GO, GO:0016021, C:integral to membrane, IEA.
GO, GO:0019028, C:viral capsid; IEA.
GO, GO:0019021, C:viral capsid; IEA.
GO, GO:00190219; C:viral envelope; IEA.
InterPro; IPR011010; DNA brk join_enz.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
PFin; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                   42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Lactobacillales; Leuconostoc
NCBI TaxID=1244;
                                                                                                                                                                                                                                                                                   7 NGVHCTKNSLWGKVR----LKNMKYDQNTTYMGRLQDILL
                                                                                                                                                                                                                                 DB 2;
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ilarity 33.3%; Pred. No. 50;
Conservative 9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93120109; PubMed=8418850;
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                                                                                                                                                                                                                                                                                                                                                                         . STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leuconostoc gelidum.
Plasmid pLG7.6.
                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR.
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P34034;
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Nest Local S
                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                RESULT 15
LCCA_LEUGE
                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                             PDB; ICWG; NRR; 425-61.

PDB; 3LEU; NRR; 625-61.

PDB; 3LEU; NRR; 625-61.

PDB; 3LEU; NRR; 625-61.

InterPro; IPR002633; Bacteriocin_II.

InterPro; IPR010133; Bacteriocin_II; I.

ProDom; PD04452; Bacteriocin_II; I.

ProDom; PD04452; Bacteriocin_II; I.

TIGRPAMB; TIGR01847; bacteriocin_aig; I.

3D-structure; Antibiotic; Bacteriocin, Direct protein sequencing; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6586 MW; 4A645D631486409F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriocin leucocin
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                                                                                                                                                                                                          EMBL; M64371; AAA68003.1; -.
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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